

## SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana  
Carroll, Joseph M.

<120> 23565, A NOVEL HUMAN ZINC  
CARBOXYPEPTIDASE FAMILY MEMBER AND USES THEREOF

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<150> 60/269, 440

<151> 2001-02-16

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 Met Gln Gly Thr Pro  
 1 5

ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg aat ttc 270  
 Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met Asn Phe  
 25 30 35

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aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag cag ctt      318
Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys Gln Leu
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Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val Asp Phe
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tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga gtt cct 414  
Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg Val Pro

70

75

80

85

ttc tcc gaa ctg aaa gac atc aaa gct tat ctg gag tct cat gga ctt				462
Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu Glu Ser His Gly Leu				
90	95	100		
gct tac agc atc atg ata aag gac atc cag gtg ctg ctg gat gag gaa				510
Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val Leu Leu Asp Glu Glu				
105	110	115		
aga cag gcc atg gcg aaa tcc cgc cg <sup>g</sup> ctg gag cgc agc acc aac agc				558
Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu Arg Ser Thr Asn Ser				
120	125	130		
ttc agt tac tca tca tac cac acc ctg gag gag ata tat agc tgg att				606
Phe Ser Tyr Ser Ser Tyr His Thr Leu Glu Glu Ile Tyr Ser Trp Ile				
135	140	145		
gac aac ttt gta atg gag cat tcc gat att gtc tca aaa att cag att				654
Asp Asn Phe Val Met Glu His Ser Asp Ile Val Ser Lys Ile Gln Ile				
150	155	160	165	
ggc aac agc ttt gaa aac cag tcc att ctt gtc ctg aag ttc agc act				702
Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val Leu Lys Phe Ser Thr				
170	175	180		
gga ggt tct cgg cac cca gcc atc tgg atc gac act gga att cac tcc				750
Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp Thr Gly Ile His Ser				
185	190	195		
cgg gag tgg atc acc cat gcc acc ggc atc tgg act gcc aat aag att				798
Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp Thr Ala Asn Lys Ile				
200	205	210		
gtc agt gat tat ggc aaa gac cgt gtc ctg aca gac ata ctg aat gcc				846
Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr Asp Ile Leu Asn Ala				
215	220	225		
atg gac atc ttc ata gag ctc gtc aca aac cct gat ggg ttt gct ttt				894
Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro Asp Gly Phe Ala Phe				
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acc cac agc atg aac cgc tta tgg cgg aag aac aag tcc atc aga cct				942
Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn Lys Ser Ile Arg Pro				
250	255	260		
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Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg Asn Trp Lys Ser Gly				
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Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys Ser Glu Thr Tyr His				
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Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala Ala Ile Val Asn Phe				
295	300	305		

atc aca gcc cat ggc aac ttc aag gct ctg atc tcc atc cac agc tac Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile Ser Ile His Ser Tyr 310 315 320 325	1134
tct cag atg ctt atg tac cct tac ggc cga ttg ctg gag ccc gtt tca Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu Leu Glu Pro Val Ser 330 335 340	1182
aat cag agg gag ttg tac gat ctt gcc aag gat gcg gtg gag gcc ttg Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp Ala Val Glu Ala Leu 345 350 355	1230
tat aag gtc cat ggg atc gag tac att ttt ggc agc atc agc acc acc Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly Ser Ile Ser Thr Thr 360 365 370	1278
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ttc ctg ctg ccg gcc aca cag atc atc ccc acg gcc cag gag acg tgg Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr Ala Gln Glu Thr Trp 410 415 420	1422
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Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro 50 55 60	
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val 65 70 75 80	
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu 85 90 95	
Glu Ser His Gly Leu Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val	

100	105	110													
Leu	Leu	Asp	Glu	Glu	Arg	Gln	Ala	Met	Ala	Lys	Ser	Arg	Arg	Leu	Glu
115							120					125			
Arg	Ser	Thr	Asn	Ser	Phe	Ser	Tyr	Ser	Ser	Tyr	His	Thr	Leu	Glu	Glu
130							135				140				
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145					150					155			160		
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Leu	Lys	Phe	Ser	Thr	Gly	Gly	Ser	Arg	His	Pro	Ala	Ile	Trp	Ile	Asp
					180			185				190			
Thr	Gly	Ile	His	Ser	Arg	Glu	Trp	Ile	Thr	His	Ala	Thr	Gly	Ile	Trp
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					210			215			220				
Asp	Ile	Leu	Asn	Ala	Met	Asp	Ile	Phe	Ile	Glu	Leu	Val	Thr	Asn	Pro
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Asp	Gly	Phe	Ala	Phe	Thr	His	Ser	Met	Asn	Arg	Leu	Trp	Arg	Lys	Asn
					245			250			255				
Lys	Ser	Ile	Arg	Pro	Gly	Ile	Phe	Cys	Ile	Gly	Val	Asp	Leu	Asn	Arg
					260			265			270				
Asn	Trp	Lys	Ser	Gly	Phe	Gly	Gly	Asn	Gly	Ser	Asn	Ser	Asn	Pro	Cys
					275			280			285				
Ser	Glu	Thr	Tyr	His	Gly	Pro	Ser	Pro	Gln	Ser	Glu	Ser	Glu	Val	Ala
					290			295			300				
Ala	Ile	Val	Asn	Phe	Ile	Thr	Ala	His	Gly	Asn	Phe	Lys	Ala	Leu	Ile
					305			310			315			320	
Ser	Ile	His	Ser	Tyr	Ser	Gln	Met	Leu	Met	Tyr	Pro	Tyr	Gly	Arg	Leu
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Leu	Glu	Pro	Val	Ser	Asn	Gln	Arg	Glu	Leu	Tyr	Asp	Leu	Ala	Lys	Asp
					340			345			350				
Ala	Val	Glu	Ala	Leu	Tyr	Lys	Val	His	Gly	Ile	Glu	Tyr	Ile	Phe	Gly
					355			360			365				
Ser	Ile	Ser	Thr	Thr	Leu	Tyr	Val	Ala	Ser	Gly	Ile	Thr	Val	Asp	Trp
					370			375			380				
Ala	Tyr	Asp	Ser	Gly	Ile	Lys	Tyr	Ala	Phe	Ser	Phe	Glu	Leu	Arg	Asp
					385			390			395			400	
Thr	Gly	Gln	Tyr	Gly	Phe	Leu	Leu	Pro	Ala	Thr	Gln	Ile	Ile	Pro	Thr
					405			410			415				
Ala	Gln	Glu	Thr	Trp	Met	Ala	Leu	Arg	Thr	Ile	Met	Glu	His	Thr	Leu
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Asn	His	Pro	Tyr												
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cttgcttaca	gcatcatgt	aaaggacatc	caggtgctgc	tggatgagga	aagacaggcc	360
atggcgaaat	cccgccggct	ggagcgcagc	accaacagct	tca	tactc	420

accctggagg	agatata tag	ctggattgac	aactt gta a	tggagcattc	cgatattgtc	480
tcaaaaattc	agattggcaa	cagctt gaa	aaccagtcc a	ttcttgcct	gaagttcagc	540
actggaggtt	ctcgccaccc	agccatctgg	atcgacactg	gaattcactc	ccgggagtgg	600
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gatgggtttg	cttttaccca	cagcatgaac	cgcttatggc	ggaagaacaa	gtccatcaga	780
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&lt;212&gt; PRT

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&lt;220&gt;

&lt;223&gt; Consensus sequence

&lt;400&gt; 4

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					20				25					30	
Gly	Arg	Asp	Leu	Lys	Val	Leu	Lys	Ile	Ser	Asp	Asn	Pro	Ala	Thr	Gly
					35			40				45			
Glu	Asn	Glu	Pro	Glu	Val	Phe	Ala	Val	Ala	Gly	Trp	Ile	His	Ala	Arg
					50			55			60				
Glu	Trp	Val	Thr	Ser	Ala	Thr	Leu	Leu	Trp	Leu	Leu	Lys	Glu	Leu	Val
					65			70			75		80		
Ala	Asn	Tyr	Gly	Ser	Asp	Lys	Thr	Ile	Thr	Lys	Leu	Leu	Asp	Gly	Leu
					85				90			95			
Asp	Leu	Phe	Tyr	Ile	Leu	Pro	Val	Phe	Asn	Pro	Asp	Gly	Tyr	Ala	Tyr
					100				105			110			
Ser	Ile	Thr	Thr	Asp	Ser	Tyr	Arg	Met	Trp	Arg	Lys	Thr	Arg	Ser	Pro
					115				120			125			
Asn	Ala	Gly	Ser	Phe	Cys	Val	Gly	Thr	Asp	Pro	Asn	Arg	Asn	Trp	Tyr
					130			135			140				
Ala	Gln	Trp	Gly	Gly	Met	Gly	Ala	Ser	Ser	Tyr	Ser	Pro	Cys	Ser	Glu
					145			150			155		160		
Thr	Tyr	Glu	Gly	Thr	Ala	Pro	Phe	Ser	Glu	Pro	Glu	Thr	Lys	Ala	Val
					165			170			175				
Glu	Asp	Phe	Ile	Arg	Ser	Trp	Leu	Gly	Gly	Lys	Gln	Asn	Ile	Lys	
					180			185			190				
Ala	Tyr	Ile	Thr	Phe	His	Ser	Tyr	Ser	Gln	Leu	Leu	Leu	Tyr	Pro	Tyr
					195			200			205				
Gly	Tyr	Asp	Tyr	Asn	Leu	Asn	Pro	Asp	Ala	Asn	Asp	Leu	Asp	Glu	Leu
					210			215			220				
Ser	Asp	Leu	Lys	Ile	Ala	Ala	Asp	Ala	Leu	Ser	Ala	Arg	His	Gly	Thr
					225			230			235		240		
Tyr	Tyr	Thr	Leu	Gly	Leu	Pro	Gly	Ser	Ser	Thr	Ile	Tyr	Pro	Ala	Ser
					245			250			255				

Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp Val Gly Ile Ile Lys Tyr  
 260 265 270  
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 Cys Phe Leu Leu Pro Glu Glu Gln Ile Ile Pro Thr Gly Ser Glu Glu  
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 Tyr Glu Gly Arg Pro Ile Lys Val Leu Lys Ile Lys Pro Ala Val Phe  
 35 40 45  
 Ile Asp Ala Gly Ile His Ala Arg Glu Trp Ile Ala Pro Ala Thr Ala  
 50 55 60  
 Leu Tyr Leu Ile Asn Gln Leu Leu Thr Asn Glu Thr Glu Tyr Ser Lys  
 65 70 75 80  
 Asp Pro Asp Asp Glu Gly Ser Val Thr Lys Leu Leu Asp Lys Leu Asp  
 85 90 95  
 Trp Tyr Ile Val Pro Val Met Asn Pro Asp Gly Tyr Glu Tyr Thr His  
 100 105 110  
 Thr Ser Thr Asp Arg Leu Trp Arg Lys Asn Arg Ser Pro Asn Gly Ala  
 115 120 125  
 Ser Gly Ser Gln Gly Thr Trp Tyr Asn Cys Tyr Gly Val Asp Leu Asn  
 130 135 140  
 Arg Asn Phe Asp Phe His Asn Trp Gly Glu Ile Gly Ser Ser Ser  
 145 150 155 160  
 Leu Pro Cys Ser Glu Thr Tyr Ala Gly Ser Ser Pro Phe Ser Glu Trp  
 165 170 175  
 Glu Pro Glu Thr Lys Ala Leu Leu Asp Phe Ile Leu Ser Asn Glu Ile  
 180 185 190  
 Gly Lys Gly Arg Ile Lys Ala Tyr Ile Ser Leu His Ser Tyr Ser Gln  
 195 200 205  
 Leu Leu Leu Tyr Pro Tyr Gly Tyr Thr Asn Ala Thr Val Pro Pro Asn  
 210 215 220  
 Gly Glu Asp Leu His Lys Glu Val Ala Lys Ala Ala Lys Ala Ile  
 225 230 235 240  
 Gly Asp Tyr Tyr Phe Gly Gly Thr Leu Tyr Thr Pro Gly Ser Ser Ser  
 245 250 255  
 Ala Asp Pro Asp Leu Asp Ile Thr Leu Tyr Pro Ala Ser Gly Gly Ser  
 260 265 270  
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 275 280 285  
 Ile Glu Leu Arg Asp Thr Gly Asp Asp Ala Gly Arg Tyr Gly Phe Leu  
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  20          25          30
Asp Ser Ala Thr Pro Ile Lys Pro Gly Ser Thr Val Asp Phe Arg Val
  35          40          45
Pro Ala Glu Asp Ile Gln Ala Val Lys Ser Phe Leu Glu Gln Ser Gly
  50          55          60
Ile His Tyr Glu Val Leu Ile Glu Asp Val Gln Glu Leu Leu Glu Glu
  65          70          75          80
Gln Phe

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the *Journal of the Royal Society of Medicine* (1962, 55, 101-102) and the *Journal of Clinical Pathology* (1962, 16, 271-272).